Kuldip Paliwal

List of Publications by Year
in descending order

41 papers	3,366 citations	236833 25 h-index	330025 37 g-index
43 all docs	43 docs citations	43 times ranked	2789 citing authors

#	Article	IF	Citations
1	SPOT-Contact-LM: improving single-sequence-based prediction of protein contact map using a transformer language model. Bioinformatics, 2022, 38, 1888-1894.	1.8	25
2	Reaching alignment-profile-based accuracy in predicting protein secondary and tertiary structural properties without alignment. Scientific Reports, 2022, 12, 7607.	1.6	14
3	On The Use of Discrete Cosine Transform Polarity Spectrum in Speech Enhancement. , 2021, , .		1
4	RNA Backbone Torsion and Pseudotorsion Angle Prediction Using Dilated Convolutional Neural Networks. Journal of Chemical Information and Modeling, 2021, 61, 2610-2622.	2.5	12
5	SPOT-1D-Single: improving the single-sequence-based prediction of protein secondary structure, backbone angles, solvent accessibility and half-sphere exposures using a large training set and ensembled deep learning. Bioinformatics, 2021, 37, 3464-3472.	1.8	22
6	SPOT-1D2: Improving Protein Secondary Structure Prediction using High Sequence Identity Training Set and an Ensemble of Recurrent and Residual-convolutional Neural Networks. , 2021, , .		1
7	Identifying molecular recognition features in intrinsically disordered regions of proteins by transfer learning. Bioinformatics, 2020, 36, 1107-1113.	1.8	37
8	DEPICTER: Intrinsic Disorder and Disorder Function Prediction Server. Journal of Molecular Biology, 2020, 432, 3379-3387.	2.0	46
9	SPOTâ€Fold: Fragmentâ€Free Protein Structure Prediction Guided by Predicted Backbone Structure and Contact Map. Journal of Computational Chemistry, 2020, 41, 745-750.	1.5	9
10	RNA secondary structure prediction using an ensemble of two-dimensional deep neural networks and transfer learning. Nature Communications, 2019, 10, 5407.	5.8	214
11	Improving prediction of protein secondary structure, backbone angles, solvent accessibility and contact numbers by using predicted contact maps and an ensemble of recurrent and residual convolutional neural networks. Bioinformatics, 2019, 35, 2403-2410.	1.8	145
12	Sixty-five years of the long march in protein secondary structure prediction: the final stretch?. Briefings in Bioinformatics, 2018, 19, bbw129.	3.2	168
13	Accurate Single-Sequence Prediction of Protein Intrinsic Disorder by an Ensemble of Deep Recurrent and Convolutional Architectures. Journal of Chemical Information and Modeling, 2018, 58, 2369-2376.	2.5	67
14	Singleâ€sequenceâ€based prediction of protein secondary structures and solvent accessibility by deep wholeâ€sequence learning. Journal of Computational Chemistry, 2018, 39, 2210-2216.	1.5	84
15	Detecting Proline and Non-Proline Cis Isomers in Protein Structures from Sequences Using Deep Residual Ensemble Learning. Journal of Chemical Information and Modeling, 2018, 58, 2033-2042.	2.5	13
16	Accurate prediction of protein contact maps by coupling residual two-dimensional bidirectional long short-term memory with convolutional neural networks. Bioinformatics, 2018, 34, 4039-4045.	1.8	155
17	Improving protein disorder prediction by deep bidirectional long short-term memory recurrent neural networks. Bioinformatics, 2017, 33, 685-692.	1.8	235
18	Capturing non-local interactions by long short-term memory bidirectional recurrent neural networks for improving prediction of protein secondary structure, backbone angles, contact numbers and solvent accessibility. Bioinformatics, 2017, 33, 2842-2849.	1.8	300

#	Article	IF	Citations
19	SPIDER2: A Package to Predict Secondary Structure, Accessible Surface Area, and Main-Chain Torsional Angles by Deep Neural Networks. Methods in Molecular Biology, 2017, 1484, 55-63.	0.4	137
20	Phase distortion resulting in a just noticeable difference in the perceived quality of speech. Speech Communication, 2016, 81, 138-147.	1.6	10
21	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. Bioinformatics, 2016, 32, 843-849.	1.8	79
22	Importance of dimensionality reduction in protein fold recognition. , 2015, , .		1
23	Predict Gram-Positive and Gram-Negative Subcellular Localization via Incorporating Evolutionary Information and Physicochemical Features Into Chou's General PseAAC. IEEE Transactions on Nanobioscience, 2015, 14, 915-926.	2.2	72
24	Improving prediction of secondary structure, local backbone angles and solvent accessible surface area of proteins by iterative deep learning. Scientific Reports, 2015, 5, 11476.	1.6	290
25	Advancing the Accuracy of Protein Fold Recognition by Utilizing Profiles From Hidden Markov Models. IEEE Transactions on Nanobioscience, 2015, 14, 761-772.	2.2	34
26	Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Chou×³s general PseAAC. Journal of Theoretical Biology, 2015, 364, 284-294.	0.8	232
27	Modulation Processing for Speech Enhancement. , 2015, , 319-345.		1
28	Using STFT real and imaginary parts of modulation signals for MMSE-based speech enhancement. Speech Communication, 2014, 58, 49-68.	1.6	25
29	Proposing a highly accurate protein structural class predictor using segmentation-based features. BMC Genomics, 2014, 15, S2.	1.2	32
30	Predicting backbone CÎ± angles and dihedrals from protein sequences by stacked sparse autoâ€encoder deep network. Journal of Computational Chemistry, 2014, 35, 2040-2046.	1.5	133
31	A Segmentation-Based Method to Extract Structural and Evolutionary Features for Protein Fold Recognition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 510-519.	1.9	34
32	A Combination of Feature Extraction Methods with an Ensemble of Different Classifiers for Protein Structural Class Prediction Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 564-575.	1.9	53
33	Protein Fold Recognition Using an Overlapping Segmentation Approach and a Mixture of Feature Extraction Models. Lecture Notes in Computer Science, 2013, , 32-43.	1.0	7
34	Enhancing Protein Fold Prediction Accuracy Using Evolutionary and Structural Features. Lecture Notes in Computer Science, 2013, , 196-207.	1.0	21
35	Exploring Potential Discriminatory Information Embedded in PSSM to Enhance Protein Structural Class Prediction Accuracy. Lecture Notes in Computer Science, 2013, , 208-219.	1.0	12
36	Speech enhancement using a minimum mean-square error short-time spectral modulation magnitude estimator. Speech Communication, 2012, 54, 282-305.	1.6	54

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37	The importance of phase in speech enhancement. Speech Communication, 2011, 53, 465-494.	1.6	326
38	Role of modulation magnitude and phase spectrum towards speech intelligibility. Speech Communication, 2011, 53, 327-339.	1.6	23
39	Single-channel speech enhancement using spectral subtraction in the short-time modulation domain. Speech Communication, 2010, 52, 450-475.	1.6	146
40	Effect of Analysis Window Duration on Speech Intelligibility. IEEE Signal Processing Letters, 2008, 15, 785-788.	2.1	33
41	Exploiting Conjugate Symmetry of the Short-Time Fourier Spectrum for Speech Enhancement. IEEE Signal Processing Letters, 2008, 15, 461-464.	2.1	58